

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

What is claimed is:

1-48. (Cancelled)

49. (Currently Amended) A peptide consisting of the formula V, $RX_6X_7X_8X_9$ (SEQ ID No. 293),

wherein

X_6 is arginine, serine or lysine;

X_7 is leucine, isoleucine or valine;

X_8 is asparagine, alanine, glycine or isoleucine; and

X_9 is phenylalanine;

or variants thereof.

50. (Currently Amended) A peptide consisting of the formula V,

$RX_6X_7X_8X_9$ (SEQ ID No. 293) or variants thereof,

wherein:

(a) R is unchanged or conservatively substituted by a basic amino acid;

(b) X_6 is ~~substituted by~~ arginine, serine or lysine or any amino acid capable of providing at least one site for participating in hydrogen bonding;

(c) X_7 is ~~unchanged~~ leucine, isoleucine or valine or conservatively substituted;

(d) X_8 is ~~unchanged~~ asparagine, alanine, glycine or isoleucine or conservatively substituted; or

(e) X_9 is ~~unchanged~~ phenylalanine or substituted by any aromatic amino acid.

51. (Currently Amended) A peptide consisting of the ~~according to~~ formula V,

$RX_6X_7X_8X_9$ (SEQ ID No. 293) or variants thereof,

wherein:

(a) R is replaced by either a basic residue or an uncharged natural or unnatural amino acid residue;

(b) X₆ is arginine, serine or lysine or is replaced by a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage;

(c) X₇ is leucine, isoleucine or valine or is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain;

(d) X₈ is asparagine, alanine, glycine or isoleucine or is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain; or

(e) X₉ is phenylalanine or is replaced with a natural or unnatural amino acid.

52. **(Previously Presented)** The peptide of claim 50, wherein R is unchanged or conservatively substituted by a basic amino acid.

53. **(Previously Presented)** The peptide of claim 50, wherein X₆ is substituted by any amino acid capable of providing at least one site for participating in hydrogen bonding.

54. **(Previously Presented)** The peptide of claim 50, wherein X₇ is unchanged or conservatively substituted.

55. **(Previously Presented)** The peptide of claim 50, wherein X₈ is unchanged or conservatively substituted.

56. **(Previously Presented)** The peptide of claim 50, wherein X₉ is unchanged or substituted by any aromatic amino acid.

57. **(Previously Presented)** The peptide of claim 51, wherein R is replaced by either a basic residue or an uncharged natural or unnatural amino acid residue.

58. **(Previously Presented)** The peptide of claim 57, wherein the basic residue is lysine.

59. **(Previously Presented)** The peptide of claim 57, wherein the uncharged natural or unnatural amino acid residue is selected from the group consisting of citrulline (Cit), homoserine, histidine, norleucine (Nle) and glutamine.
60. **(Previously Presented)** The peptide of claim 51, wherein X_6 is replaced by a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage.
61. **(Previously Presented)** The peptide of claim 60, wherein the natural or unnatural amino acid residue is selected from the group consisting of asparagine, proline, aminoisobutyric acid (Aib) and sarcosine (Sar).
62. **(Previously Presented)** The peptide of claim 60, wherein the amino acid residue capable of forming a cyclic linkage is ornithine.
63. **(Previously Presented)** The peptide of claim 51, wherein X_7 is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain.
64. **(Previously Presented)** The peptide of claim 63, wherein the natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain is selected from the group consisting of norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine and 1-naphthylalanine (1Nal).
65. **(Previously Presented)** The peptide of claim 51, wherein X_8 is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain.
66. **(Previously Presented)** The peptide of claim 65, wherein the natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain is selected from the group consisting of norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine and 1-naphthylalanine (1Nal).
67. **(Previously Presented)** The peptide of claim 51, wherein X_9 is replaced with a natural or unnatural amino acid.

68. **(Previously Presented)** The peptide of claim 67, wherein the natural or unnatural amino acid is selected from the group consisting of leucine, cyclohexylalanine (Cha), homophenylalanine (Hof), tyrosine, para-fluorophenylalanine (pFPhe), meta-fluorophenylalanine (mFPhe), tryptophan, 1-naphthylalanine (1Nal), 2-naphthylalanine (2Nal), meta-chlorophenylalanine (mClPhe), biphenylalanine (Bip) and 1,2,3,4-Tetrahydroisoquinoline-3-carboxylic acid (Tic).

69. **(Previously Presented)** The peptide as in any of claims 49-51, wherein the N-terminal is acylated.

70. **(Previously Presented)** The peptide as in any of claims 49-51, wherein R is substituted by citrulline.

71. **(Previously Presented)** A peptide selected from the group consisting of:

H-	Arg	Arg	Leu	Asn	Phe	NH ₂	(SEQ ID No. 294)
H-	Arg	Arg	Leu	Asn	PFF	NH ₂	(SEQ ID No. 295)
H-	Arg	Arg	Leu	Asn	MCIF	NH ₂	(SEQ ID No. 296)
H-	Arg	Arg	Leu	Ala	Phe	NH ₂	(SEQ ID No. 297)
H-	Arg	Arg	Leu	Ala	PFF	NH ₂	(SEQ ID No. 298)
H-	Arg	Arg	Leu	Ala	MCIF	NH ₂	(SEQ ID No. 299)
H-	Arg	Arg	Leu	Gly	Phe	NH ₂	(SEQ ID No. 300)
H-	Arg	Arg	Leu	Gly	pFF	NH ₂	(SEQ ID No. 301)
H-	Arg	Arg	Leu	Gly	mClF	NH ₂	(SEQ ID No. 302)
H-	Arg	Arg	Ile	Asn	Phe	NH ₂	(SEQ ID No. 303)
H-	Arg	Arg	Ile	Asn	pFF	NH ₂	(SEQ ID No. 304)
H-	Arg	Arg	Ile	Asn	mClF	NH ₂	(SEQ ID No. 305)
H-	Arg	Arg	Ile	Ala	Phe	NH ₂	(SEQ ID No. 306)
H-	Arg	Arg	Ile	Ala	pFF	NH ₂	(SEQ ID No. 307)
H-	Arg	Arg	Ile	Ala	mClF	NH ₂	(SEQ ID No. 308)
H-	Arg	Arg	Ile	Gly	Phe	NH ₂	(SEQ ID No. 309)
H-	Arg	Arg	Ile	Gly	pFF	NH ₂	(SEQ ID No. 310)
H-	Arg	Arg	Ile	Gly	mClF	NH ₂	(SEQ ID No. 311)
H-	Arg	Arg	Val	Asn	Phe	NH ₂	(SEQ ID No. 312)
H-	Arg	Arg	Val	Asn	pFF	NH ₂	(SEQ ID No. 313)
H-	Arg	Arg	Val	Asn	mClF	NH ₂	(SEQ ID No. 314)
H-	Arg	Arg	Val	Ala	Phe	NH ₂	(SEQ ID No. 315)

H-	Arg	Arg	Val	Ala	pFF	NH ₂	(SEQ ID No. 316)
H-	Arg	Arg	Val	Ala	mClF	NH ₂	(SEQ ID No. 317)
H-	Arg	Arg	Val	Gly	Phe	NH ₂	(SEQ ID No. 318)
H-	Arg	Arg	Val	Gly	pFF	NH ₂	(SEQ ID No. 319)
H-	Arg	Arg	Val	Gly	mClF	NH ₂	(SEQ ID No. 320)
H-	Arg	Ser	Leu	Asn	Phe	NH ₂	(SEQ ID No. 321)
H-	Arg	Ser	Leu	Asn	pFF	NH ₂	(SEQ ID No. 322)
H-	Arg	Ser	Leu	Asn	mClF	NH ₂	(SEQ ID No. 323)
H-	Arg	Ser	Leu	Ala	Phe	NH ₂	(SEQ ID No. 324)
H-	Arg	Ser	Leu	Ala	pFF	NH ₂	(SEQ ID No. 325)
H-	Arg	Ser	Leu	Ala	mClF	NH ₂	(SEQ ID No. 326)
H-	Arg	Ser	Leu	Gly	Phe	NH ₂	(SEQ ID No. 327)
H-	Arg	Ser	Leu	Gly	pFF	NH ₂	(SEQ ID No. 328)
H-	Arg	Ser	Leu	Gly	mClF	NH ₂	(SEQ ID No. 329)
H-	Arg	Ser	Ile	Asn	Phe	NH ₂	(SEQ ID No. 330)
H-	Arg	Ser	Ile	Asn	pFF	NH ₂	(SEQ ID No. 331)
H-	Arg	Ser	Ile	Asn	mClF	NH ₂	(SEQ ID No. 332)
H-	Arg	Ser	Ile	Ala	Phe	NH ₂	(SEQ ID No. 333)
H-	Arg	Ser	Ile	Ala	pFF	NH ₂	(SEQ ID No. 334)
H-	Arg	Ser	Ile	Ala	mClF	NH ₂	(SEQ ID No. 335)
H-	Arg	Ser	Ile	Gly	Phe	NH ₂	(SEQ ID No. 336)
H-	Arg	Ser	Ile	Gly	pFF	NH ₂	(SEQ ID No. 337)
H-	Arg	Ser	Ile	Gly	mClF	NH ₂	(SEQ ID No. 338)
H-	Arg	Ser	Val	Asn	Phe	NH ₂	(SEQ ID No. 339)
H-	Arg	Ser	Val	Asn	pFF	NH ₂	(SEQ ID No. 340)
H-	Arg	Ser	Val	Asn	mClF	NH ₂	(SEQ ID No. 341)
H-	Arg	Ser	Val	Ala	Phe	NH ₂	(SEQ ID No. 342)
H-	Arg	Ser	Val	Ala	pFF	NH ₂	(SEQ ID No. 343)
H-	Arg	Ser	Val	Ala	mClF	NH ₂	(SEQ ID No. 344)
H-	Arg	Ser	Val	Gly	Phe	NH ₂	(SEQ ID No. 345)
H-	Arg	Ser	Val	Gly	pFF	NH ₂	(SEQ ID No. 346)
H-	Arg	Ser	Val	Gly	mClF	NH ₂	(SEQ ID No. 347)
H-	Arg	Lys	Leu	Asn	Phe	NH ₂	(SEQ ID No. 348)
H-	Arg	Lys	Leu	Asn	pFF	NH ₂	(SEQ ID No. 349)
H-	Arg	Lys	Leu	Asn	mClF	NH ₂	(SEQ ID No. 350)
H-	Arg	Lys	Leu	Ala	Phe	NH ₂	(SEQ ID No. 351)
H-	Arg	Lys	Leu	Ala	pFF	NH ₂	(SEQ ID No. 352)
H-	Arg	Lys	Leu	Ala	mClF	NH ₂	(SEQ ID No. 353)
H-	Arg	Lys	Leu	Gly	Phe	NH ₂	(SEQ ID No. 354)
H-	Arg	Lys	Leu	Gly	pFF	NH ₂	(SEQ ID No. 355)
H-	Arg	Lys	Leu	Gly	mClF	NH ₂	(SEQ ID No. 356)
H-	Arg	Lys	Ile	Asn	Phe	NH ₂	(SEQ ID No. 357)
H-	Arg	Lys	Ile	Asn	pFF	NH ₂	(SEQ ID No. 358)
H-	Arg	Lys	Ile	Asn	mClF	NH ₂	(SEQ ID No. 359)

H-	Arg	Lys	Ile	Ala	Phe	NH ₂	(SEQ ID No. 360)
H-	Arg	Lys	Ile	Ala	pFF	NH ₂	(SEQ ID No. 361)
H-	Arg	Lys	Ile	Ala	mClF	NH ₂	(SEQ ID No. 362)
H-	Arg	Lys	Ile	Gly	Phe	NH ₂	(SEQ ID No. 363)
H-	Arg	Lys	Ile	Gly	pFF	NH ₂	(SEQ ID No. 364)
H-	Arg	Lys	Ile	Gly	mClF	NH ₂	(SEQ ID No. 365)
H-	Arg	Lys	Val	Asn	Phe	NH ₂	(SEQ ID No. 366)
H-	Arg	Lys	Val	Asn	pFF	NH ₂	(SEQ ID No. 367)
H-	Arg	Lys	Val	Asn	mClF	NH ₂	(SEQ ID No. 368)
H-	Arg	Lys	Val	Ala	Phe	NH ₂	(SEQ ID No. 369)
H-	Arg	Lys	Val	Ala	pFF	NH ₂	(SEQ ID No. 370)
H-	Arg	Lys	Val	Ala	mClF	NH ₂	(SEQ ID No. 371)
H-	Arg	Lys	Val	Gly	Phe	NH ₂	(SEQ ID No. 372)
H-	Arg	Lys	Val	Gly	pFF	NH ₂	(SEQ ID No. 373)
H-	Arg	Lys	Val	Gly	mClF	NH ₂	(SEQ ID No. 374)
H-	Arg	Arg	Leu	Ile	pFF	NH ₂	(SEQ ID No. 375)
H-	Cit	Cit	Leu	Ile	pFF	NH ₂	(SEQ ID No. 376)
H-	Arg	Arg	Leu	Ile	Phe	NH ₂	(SEQ ID No. 377)

72. **(Previously Presented)** The peptide of claim 71, wherein the peptide is selected from the group consisting of:

H-	Arg	Arg	Leu	Asn	Phe	NH ₂	(SEQ ID No. 294)
H-	Arg	Arg	Leu	Asn	PFF	NH ₂	(SEQ ID No. 295)
H-	Arg	Arg	Leu	Asn	MCIF	NH ₂	(SEQ ID No. 296)
H-	Arg	Arg	Leu	Ala	PFF	NH ₂	(SEQ ID No. 298)
H-	Arg	Arg	Leu	Ala	MCIF	NH ₂	(SEQ ID No. 299)
H-	Arg	Arg	Leu	Gly	PFF	NH ₂	(SEQ ID No. 301)
H-	Arg	Arg	Leu	Gly	MCIF	NH ₂	(SEQ ID No. 302)
H-	Arg	Arg	Ile	Asn	PFF	NH ₂	(SEQ ID No. 304)
H-	Arg	Arg	Ile	Asn	MCIF	NH ₂	(SEQ ID No. 305)
H-	Arg	Arg	Ile	Ala	PFF	NH ₂	(SEQ ID No. 307)
H-	Arg	Arg	Ile	Ala	MCIF	NH ₂	(SEQ ID No. 308)
H-	Arg	Lys	Leu	Asn	MCIF	NH ₂	(SEQ ID No. 350)
H-	Arg	Lys	Leu	Ala	PFF	NH ₂	(SEQ ID No. 352)
H-	Arg	Lys	Leu	Ala	MCIF	NH ₂	(SEQ ID No. 353)
H-	Arg	Lys	Leu	Gly	PFF	NH ₂	(SEQ ID No. 355)
H-	Arg	Lys	Ile	Asn	PFF	NH ₂	(SEQ ID No. 358)
H-	Arg	Arg	Leu	Ile	PFF	NH ₂	(SEQ ID No. 375)

73. **(Previously Presented)** The peptide of claim 71, wherein the peptide is selected from the group consisting of:

H-	Arg	Arg	Leu	Asn	Phe	NH ₂	(SEQ ID No. 294)
H-	Arg	Arg	Leu	Asn	PFF	NH ₂	(SEQ ID No. 295)
H-	Arg	Arg	Leu	Asn	MCIF	NH ₂	(SEQ ID No. 296)
H-	Arg	Arg	Leu	Ala	PFF	NH ₂	(SEQ ID No. 298)
H-	Arg	Arg	Leu	Ala	MCIF	NH ₂	(SEQ ID No. 299)
H-	Arg	Arg	Leu	Gly	PFF	NH ₂	(SEQ ID No. 301)
H-	Arg	Arg	Leu	Gly	MCIF	NH ₂	(SEQ ID No. 302)
H-	Arg	Arg	Ile	Asn	PFF	NH ₂	(SEQ ID No. 304)
H-	Arg	Arg	Ile	Asn	MCIF	NH ₂	(SEQ ID No. 305)
H-	Arg	Arg	Ile	Ala	PFF	NH ₂	(SEQ ID No. 307)
H-	Arg	Arg	Ile	Ala	MCIF	NH ₂	(SEQ ID No. 308)
H-	Arg	Lys	Leu	Asn	MCIF	NH ₂	(SEQ ID No. 350)
H-	Arg	Lys	Leu	Ala	PFF	NH ₂	(SEQ ID No. 352)
H-	Arg	Lys	Leu	Ala	MCIF	NH ₂	(SEQ ID No. 353)
H-	Arg	Lys	Leu	Gly	PFF	NH ₂	(SEQ ID No. 355)
H-	Arg	Lys	Ile	Asn	PFF	NH ₂	(SEQ ID No. 358)
H-	Arg	Arg	Leu	Ile	PFF	NH ₂	(SEQ ID No. 375)